

## SEQUENCE LISTING

<110> OSTERMEIER, MARC A.  
GUNTAS, GURKAN

<120> METHODS FOR MAKING AND USING MOLECULAR SWITCHES  
INVOLVING CIRCULAR PERMUTATION

<130> 71699/62568

<140> 10/588,114

<141> 2006-07-27

<150> PCT/US05/002633

<151> 2005-01-28

<150> 60/628,997

<151> 2004-11-18

<150> 60/607,684

<151> 2004-09-07

<150> 60/557,152

<151> 2004-03-26

<150> 60/539,774

<151> 2004-01-28

<160> 99

<170> PatentIn Ver. 3.3

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
peptide linker

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Gly Ser Gly Gly Gly  
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<210> 2

<211> 37

<212> PRT

<213> Homo sapiens

<400> 2

Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser  
1 5 10 15

Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr  
20 25 30

Met Gly Leu Leu Thr  
35

<210> 3  
<211> 14  
<212> PRT  
<213> Rous sarcoma virus

<400> 3  
Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg  
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<210> 4  
<211> 25  
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<213> Unknown Organism

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<223> Description of Unknown Organism: GRK6 peptide  
sequence

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Leu Leu Gln Arg Leu Phe Ser Arg Gln Asp Cys Cys Gly Asn Cys Ser  
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Asp Ser Glu Glu Glu Leu Pro Thr Arg  
20 25

<210> 5  
<211> 7  
<212> PRT  
<213> Monkey virus SV40

<400> 5  
Pro Lys Lys Lys Lys Lys Val  
1 5

<210> 6  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 6  
Ala Arg Arg Arg Arg Pro  
1 5

<210> 7  
<211> 10  
<212> PRT  
<213> Unknown Organism

<220>

<223> Description of Unknown Organism: NF kappa-B p50  
sequence

<400> 7

Glu Glu Val Gln Arg Lys Arg Gln Lys Leu  
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<210> 8

<211> 9

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: NF kappa-B p65  
sequence

<400> 8

Glu Glu Lys Arg Lys Arg Thr Tyr Glu  
1 5

<210> 9

<211> 21

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Nucleoplasmin  
sequence

<400> 9

Ala Val Lys Arg Pro Ala Ala Thr Leu Lys Lys Ala Gly Gln Ala Lys  
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Lys Lys Lys Leu Asp  
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<210> 10

<211> 5

<212> PRT

<213> Homo sapiens

<400> 10

Lys Phe Glu Arg Gln  
1 5

<210> 11

<211> 36

<212> PRT

<213> Homo sapiens

<400> 11

Met Leu Ile Pro Ile Ala Gly Phe Phe Ala Leu Ala Gly Leu Val Leu  
1 5 10 15

Ile Val Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly  
                   20                  25                  30

Tyr Gln Thr Ile  
                   35

<210> 12  
 <211> 35  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
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Val Leu Leu Ala Tyr Phe Ile Gly Leu Lys His His His Ala Gly Tyr  
                   20                  25                  30

Glu Gln Phe  
                   35

<210> 13  
 <211> 27  
 <212> PRT  
 <213> Saccharomyces cerevisiae

<400> 13  
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Phe Ser Arg Asn Ile Leu Arg Leu Gln Ser Thr  
                   20                  25

<210> 14  
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 <212> PRT  
 <213> Saccharomyces cerevisiae

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Thr Leu Cys Ser Ser Arg Tyr Leu Leu  
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<210> 15  
 <211> 64  
 <212> PRT  
 <213> Saccharomyces cerevisiae

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Ser Phe Tyr Ser Thr Ala Thr Gly Ala Ala Ser Lys Ser Gly Lys Leu  
                   20                  25                  30  
 Thr Gln Lys Leu Val Thr Ala Gly Val Ala Ala Ala Gly Ile Thr Ala  
                   35                  40                  45  
 Ser Thr Leu Leu Tyr Ala Asp Ser Leu Thr Ala Glu Ala Met Thr Ala  
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<210> 16  
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 <212> PRT  
 <213> *Saccharomyces cerevisiae*

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 Ala Ala Thr Gly Thr Ala Ile Gly Ala Tyr Tyr Tyr Tyr Asn Gln Leu  
                   20                  25                  30  
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                   35                  40

<210> 17  
 <211> 4  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism: Endoplasmic  
       reticulum localizing sequence

<400> 17  
 Lys Asp Glu Leu  
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<210> 18  
 <211> 15  
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 <213> Human adenovirus type 19

<400> 18  
 Leu Tyr Leu Ser Arg Arg Ser Phe Ile Asp Glu Lys Lys Met Pro  
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<210> 19  
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 <213> Unknown Organism

<220>

<223> Description of Unknown Organism: Interleukin-2  
sequence

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Val Thr Asn Ser  
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<210> 20

<211> 29

<212> PRT

<213> Homo sapiens

<400> 20

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu  
1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr  
20 25

<210> 21

<211> 27

<212> PRT

<213> Homo sapiens

<400> 21

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Ala Leu  
1 5 10 15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn  
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<210> 22

<211> 18

<212> PRT

<213> Influenza A virus

<400> 22

Met Lys Ala Lys Leu Leu Val Leu Leu Tyr Ala Phe Val Ala Gly Asp  
1 5 10 15

Gln Ile

<210> 23

<211> 24

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Interleukin-4  
sequence

<400> 23

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Cys Ala Gly Asn Phe Val His Gly  
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<210> 24

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
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37

<210> 25

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
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<400> 25

gtctgaggat cccaatgct taatcagtga

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<210> 26

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
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gccgttaatc cagattac

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<210> 27

<211> 41

<212> DNA

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<400> 27  
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<210> 28  
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<400> 28  
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<220>  
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<210> 31  
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39

<210> 32  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
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primer

<220>  
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<400> 33  
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<210> 34  
<211> 36  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic primer

&lt;400&gt; 34

atccggacta gtaggccttt acttggtgat acgagt

36

&lt;210&gt; 35

&lt;211&gt; 1995

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;400&gt; 35

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cgtatcacca agtaa
1995

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&lt;210&gt; 36

&lt;211&gt; 664

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 36

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  1             5             10             15

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                   35                                  40                                  45  
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu  
                   50                                  55                                  60  
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly  
                   65                                  70                                  75                                  80  
 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr  
                                   85                                  90                                  95  
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln  
                                   100                                  105                                  110  
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys  
                   115                                  120                                  125  
 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn  
                   130                                  135                                  140  
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala  
                   145                                  150                                  155                                  160  
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn  
                                   165                                  170                                  175  
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly  
                                   180                                  185                                  190  
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly  
                   195                                  200                                  205  
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu  
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 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu  
                   225                                  230                                  235                                  240  
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp  
                                   245                                  250                                  255  
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val  
                   260                                  265                                  270  
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu  
                   275                                  280                                  285  
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu  
                   290                                  295                                  300  
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn  
                   305                                  310                                  315                                  320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu  
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 Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr  
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 Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met  
 370 375 380  
 Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala  
 385 390 395 400  
 Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg  
 405 410 415  
 Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val  
 420 425 430  
 Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg  
 435 440 445  
 Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser  
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 His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly  
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 Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys  
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 Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu  
 515 520 525  
 Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr  
 530 535 540  
 Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu  
 545 550 555 560  
 Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu  
 565 570 575  
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 580 585 590  
 Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu  
 595 600 605  
 Asn Glu Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met  
 610 615 620

Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala  
625 630 635 640

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Asp Ala Gln Thr Arg Ile Thr Lys  
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<211> 1989  
<212> DNA  
<213> Escherichia coli

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<210> 38  
<211> 662  
<212> PRT  
<213> Escherichia coli

&lt;400&gt; 38

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 35 40 45  
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu  
 50 55 60  
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly  
 65 70 75 80  
 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr  
 85 90 95  
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln  
 100 105 110  
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys  
 115 120 125  
 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn  
 130 135 140  
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala  
 145 150 155 160  
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn  
 165 170 175  
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 180 185 190  
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly  
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 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu  
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 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu  
 225 230 235 240  
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 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val  
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 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu  
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 Leu Ala Lys Asp Pro Arg Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr  
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 Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu  
 355 360 365  
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 Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp  
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 405 410 415  
 Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile  
 420 425 430  
 Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile  
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 Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser His Pro  
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 Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg  
 465 470 475 480  
 Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser  
 485 490 495  
 Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu  
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 Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu  
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 Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro  
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 Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys  
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 Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu  
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 580 585 590  
 Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu  
 595 600 605

Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn  
 610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile  
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Gln Thr Arg Ile Thr Lys  
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<210> 39  
 <211> 1983  
 <212> DNA  
 <213> Escherichia coli

<400> 39  
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 taa 1983



<210> 40  
 <211> 660  
 <212> PRT  
 <213> Escherichia coli

<400> 40

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Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20              25              30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35              40              45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50              55              60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65              70              75              80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
      85              90              95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100             105             110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
      115             120             125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
      130             135             140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
      145             150             155             160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
      165             170             175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
      180             185             190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
      195             200             205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
      210             215             220

Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
      225             230             235             240

Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
      245             250             255

Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
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Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu  
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 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu  
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 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn  
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 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu  
 325 330 335  
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 Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu  
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 370 375 380  
 Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile  
 385 390 395 400  
 Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala  
 405 410 415  
 Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr  
 420 425 430  
 Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu  
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 Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser His Pro Glu Thr  
 450 455 460  
 Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly  
 465 470 475 480  
 Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg  
 485 490 495  
 Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys  
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 Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg  
 515 520 525  
 Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr  
 530 535 540  
 Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala  
 545 550 555 560  
 Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr  
 565 570 575

Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp  
580 585 590

His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ala  
595 600 605

Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro  
610 615 620

Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala  
625 630 635 640

Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr  
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Arg Ile Thr Lys  
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<210> 41

<211> 1986

<212> DNA

<213> Escherichia coli

<400> 41

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aagtaa

1986

&lt;210&gt; 42

&lt;211&gt; 661

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 42

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Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
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Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
          20           25           30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35           40           45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50           55           60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65           70           75           80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
          85           90           95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
          100           105           110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
      115           120           125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
      130           135           140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
      145           150           155           160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
          165           170           175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
          180           185           190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
      195           200           205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
      210           215           220

Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
      225           230           235           240

Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
          245           250           255

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Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val
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Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu
			275				280						285		
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu
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Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn
			305				310						315		
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu
			325				330						335		
Leu	Ala	Lys	Asp	Pro	Arg	Ile	Pro	Asn	Asp	Glu	Arg	Asp	Thr	Thr	Met
			340				345						350		
Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu	Leu
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Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala	Asp
			370				375						380		
Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp	Phe
			385				390						395		
Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile
			405				410						415		
Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	Tyr
			420				425						430		
Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile	Ala
			435				440						445		
Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	His	Pro	Glu
			450				455						460		
Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val
			465				470						475		
Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe
			485				490						495		
Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu
			500				505						510		
Cys	Gly	Ala	Val	Leu	Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly
			515				520						525		
Arg	Arg	Ile	His	Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val
			530				535						540		
Thr	Glu	Lys	His	Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser
			545				550						555		

Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr  
565 570 575

Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly  
580 585 590

Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala  
595 600 605

Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile  
610 615 620

Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn  
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Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln  
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Thr Arg Ile Thr Lys  
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<210> 43

<211> 2001

<212> DNA

<213> Escherichia coli

<400> 43

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actgcgggtga tcaacgccgc cagcgggtcgt cagactgtcg atgaagccct gaaagacgcg 1980
cagactcgta tcaccaagta a                                     2001

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&lt;210&gt; 44

&lt;211&gt; 666

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 44

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Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
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Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20              25              30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35              40              45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50              55              60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65              70              75              80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
      85              90              95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100             105             110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
      115             120             125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
      130             135             140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
      145             150             155             160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
      165             170             175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
      180             185             190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
      195             200             205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asn Glu
      210             215             220

Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Ala Ala Met Ala
      225             230             235             240

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			260					265					270			
Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp	Phe	Ile	Ala	Asp	Lys	Ser	
		275					280					285				
Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	
	290					295					300					
Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	Thr	Gly	Ser	Gln	
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Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	
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Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	His	Pro	Glu	Thr	Leu	Val	Lys	Val	
			340					345					350			
Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	
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Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	
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Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu	Cys	Gly	Ala	Val	Leu	
385					390					395					400	
Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly	Arg	Arg	Ile	His	Tyr	
				405					410					415		
Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val	Thr	Glu	Lys	His	Leu	
			420					425					430			
Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser	Ala	Ala	Ile	Thr	Met	
		435					440					445				
Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	Thr	Thr	Ile	Gly	Gly	Pro	
	450					455					460					
Lys	Glu	Leu	Thr	Ala	Phe	Leu	His	Asn	Met	Gly	Asp	His	Val	Thr	Arg	
465					470					475					480	
Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu	Asn	Glu	Ala	Val	Asp	Leu	Ile	Lys	
				485					490					495		
Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	
			500					505					510			
Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	
		515					520					525				
Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	
	530					535					540					



Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser Ala  
545 550 555 560

Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu  
565 570 575

Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys Asp  
580 585 590

Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu Ala  
595 600 605

Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu  
610 615 620

Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg  
625 630 635 640

Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala  
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Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys  
660 665

<210> 45

<211> 1989

<212> DNA

<213> Escherichia coli

<400> 45

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accaagtaa                                     1989

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<210> 46

<211> 662

<212> PRT

<213> Escherichia coli

<400> 46

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Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
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Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
          20              25              30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
          35              40              45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
          50              55              60

His Pro Asp Lys Leu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
          65              70              75              80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
          85              90              95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
          100             105             110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
          115             120             125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
          130             135             140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
          145             150             155             160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
          165             170             175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
          180             185             190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
          195             200             205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
          210             215             220

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Ile Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Ala  
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 Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val  
 260 265 270  
 Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala  
 275 280 285  
 Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala  
 290 295 300  
 Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr  
 305 310 315 320  
 Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile  
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 Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser His Pro Glu Thr Leu  
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 Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr  
 355 360 365  
 Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro  
 370 375 380  
 Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly  
 385 390 395 400  
 Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg  
 405 410 415  
 Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu  
 420 425 430  
 Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala  
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 Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His  
 465 470 475 480  
 Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala His Met  
 485 490 495  
 Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly  
 500 505 510  
 Glu Thr Ala Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp  
 515 520 525

Thr Ser Lys Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly  
530 535 540

Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala  
545 550 555 560

Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu  
565 570 575

Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly  
580 585 590

Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg  
595 600 605

Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn  
610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile  
625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala  
645 650 655

Gln Thr Arg Ile Thr Lys  
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<210> 47

<211> 1989

<212> DNA

<213> Escherichia coli

<400> 47

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accaagtaa                                     1989

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&lt;210&gt; 48

&lt;211&gt; 662

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 48

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Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
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Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
          20                      25                      30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
          35                      40                      45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
          50                      55                      60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
          65                      70                      75                      80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
          85                      90                      95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
          100                     105                     110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
          115                     120                     125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
          130                     135                     140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
          145                     150                     155                     160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
          165                     170                     175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
          180                     185                     190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
          195                     200                     205

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Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	210	215	220
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	225	230	235
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	245	250	255
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	260	265	270
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	275	280	285
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	290	295	300
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	305	310	315
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	325	330	335
Leu	Ala	Lys	Asp	Pro	Arg	Asn	Glu	Ala	Ile	Pro	Asn	Asp	Glu	Arg	Asp	340	345	350
Thr	Thr	Met	Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	355	360	365
Gly	Glu	Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	370	375	380
Glu	Ala	Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	385	390	395
Gly	Trp	Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	405	410	415
Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	420	425	430
Val	Ile	Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	435	440	445
Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	450	455	460
His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	465	470	475
Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	485	490	495
Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	500	505	510

Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu  
515 520 525

Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr  
530 535 540

Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu  
545 550 555 560

Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu  
565 570 575

Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His  
580 585 590

Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu  
595 600 605

Asn Glu Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn  
610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile  
625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala  
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Gln Thr Arg Ile Thr Lys  
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<210> 49

<211> 2007

<212> DNA

<213> Escherichia coli

<400> 49

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&lt;210&gt; 50

&lt;211&gt; 668

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 50

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Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
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Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20              25              30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35              40              45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50              55              60

His Pro Asp Lys Leu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65              70              75              80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
      85              90              95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100             105             110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
      115             120             125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
      130             135             140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
      145             150             155             160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
      165             170             175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
      180             185             190

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Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly  
 195 200 205  
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu  
 210 215 220  
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu  
 225 230 235 240  
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp  
 245 250 255  
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val  
 260 265 270  
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu  
 275 280 285  
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu  
 290 295 300  
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn  
 305 310 315 320  
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu  
 325 330 335  
 Leu Ala Lys Asp Pro Arg Ile Ala Ala Thr Asn Glu Ala Ile Pro Asn  
 340 345 350  
 Asp Glu Arg Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg  
 355 360 365  
 Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu  
 370 375 380  
 Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser  
 385 390 395 400  
 Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu  
 405 410 415  
 Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro  
 420 425 430  
 Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp  
 435 440 445  
 Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His  
 450 455 460  
 Trp Asp Lys Ser His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu  
 465 470 475 480  
 Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser  
 485 490 495

Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met  
 500 505 510  
 Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp  
 515 520 525  
 Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp  
 530 535 540  
 Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met  
 545 550 555 560  
 Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr  
 565 570 575  
 Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr  
 580 585 590  
 Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp  
 595 600 605  
 Glu Pro Glu Leu Asn Glu Ala Ala Ala Thr Met Glu Asn Ala Gln Lys  
 610 615 620  
 Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala  
 625 630 635 640  
 Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp  
 645 650 655  
 Glu Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys  
 660 665

<210> 51  
 <211> 1989  
 <212> DNA  
 <213> Escherichia coli

<400> 51  
 atgaaaataa aaacaggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60  
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 aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180  
 gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240  
 gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300  
 ctggttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360  
 gatgccgtac gttacaacgg caagctgatt gcttaccgga tcgctgttga agcgttatcg 420  
 ctgatttata acaaagatct gctgccgaac ccgcaaaaaa cctgggaaga gatccccggc 480  
 ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540  
 tacttcacct ggccgctgat tgctgctgac gggggttatg cggtcaagta tgaaaacggc 600  
 aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660  
 ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcagaa 720  
 gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggg atgggtccaac 780  
 atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa ggggtcaacca 840  
 tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900  
 ctggcgaaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960  
 aaagacaaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020  
 ccacgtaatg aagccatacc aaacgacgag cgtgacacca cgatgcctgc agcaatggca 1080

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acaacgttgc gcaaactatt aactggcgaa ctacttactc tagcttcccc gcaacaatta 1140
atagactgga tggaggcgga taaagttgca ggaccacttc tgcgctcggc ccttccggct 1200
ggctgggttta ttgctgataa atctggagcc ggtgagcgtg ggtctcgcgg tatcattgca 1260
gcaactggggc cagatggtaa gccctcccgt atcgtagtta tctacacgac ggggagtcag 1320
gcaactatgg atgaacgaaa tagacagatc gctgagatag gtgcctcact gattaagcat 1380
tggaacaaga gccaccaga aacgctggtg aaagtaaaag atgctgaaga tcagtgggt 1440
gcacgagtgg gttacatcga actggatctc aacagcggta agatccttga gagttttcgc 1500
cccgaagaac gttttccaat gatgagcact tttaaagttc tgctatgtgg cgcggtatta 1560
tcccgtggtg acgccgggca agagcaactc ggtcgccgca tacactattc tcagaatgac 1620
ttggttgagt actcaccagt cacagaaaag catcttacgg atggcatgac agtaagagaa 1680
ttatgcagtg ctgccataac catgagtgat aacactgcgg ccaacttact tctgacaacg 1740
atcggaggac cgaaggagct aaccgctttt ttgcacaaca tgggggatca tgtaactcgc 1800
cttgatcggt gggaaccgga actgaatgaa gccaccatgg aaaacgcccc gaaaggtgaa 1860
atcatgccga acatcccgca gatgtccgct ttctggtatg ccgtgcgtac tgcggtgatc 1920
aacgccgcca gcggtcgtca gactgtcgat gaagccctga aagacgcgca gactcgtatc 1980
accaagtaa 1989

```

&lt;210&gt; 52

&lt;211&gt; 662

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 52

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Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1             5             10             15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
          20             25             30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
          35             40             45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
          50             55             60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
          65             70             75             80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
          85             90             95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
          100            105            110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
          115            120            125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
          130            135            140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
          145            150            155            160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
          165            170            175

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Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly  
 180 185 190  
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly  
 195 200 205  
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu  
 210 215 220  
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu  
 225 230 235 240  
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp  
 245 250 255  
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val  
 260 265 270  
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu  
 275 280 285  
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu  
 290 295 300  
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn  
 305 310 315 320  
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu  
 325 330 335  
 Leu Ala Lys Asp Pro Arg Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp  
 340 345 350  
 Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr  
 355 360 365  
 Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met  
 370 375 380  
 Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala  
 385 390 395 400  
 Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg  
 405 410 415  
 Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val  
 420 425 430  
 Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg  
 435 440 445  
 Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser  
 450 455 460  
 His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly  
 465 470 475 480

Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu  
485 490 495

Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys  
500 505 510

Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu  
515 520 525

Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr  
530 535 540

Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu  
545 550 555 560

Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu  
565 570 575

Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His  
580 585 590

Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu  
595 600 605

Asn Glu Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn  
610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile  
625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala  
645 650 655

Gln Thr Arg Ile Thr Lys  
660

&lt;210&gt; 53

&lt;211&gt; 1989

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
nucleotide construct

&lt;400&gt; 53

```

atgaaaataa aaacaggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaaactgg taatctggat taacgggcttg 120
tttggtctata acgggtctcgc tgaagtcggg aagaaattcg agaaagatac cggaattaaa 180
gtcaccggttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctatgcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggtcg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgca tcgctgttta tgcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgcaaaaaa cctgggaaga gatccggcg 480
ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttat cggttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660

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ctggttgacc tgattaaacaa caaacacatg aatgcagaca ccgattactc catcgagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccgtgggc atgggtccaac 780
atcgacacca gcaaagtga ttatgggtgta acgggtactgc cgaccttcaa ggggtcaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgtgcca taccaaacga cgagcgtgac accacgatgc ctgcagcaat ggcaacaacg 1080
ttgcgcaaac tattaactgg cgaactactt actctagctt cccggcaaca attaatagac 1140
tggatggagg cggataaagt tgcaggacca cttctgcgct cggcccttcc ggctgggtgg 1200
tttattgctg ataaatctgg agccgggtgag cgtgggtctc gcggtatcat tgcagcactg 1260
gggccagatg gtaagccctc ccgtatcgta gttatctaca cgacggggag tcaggcaact 1320
atggatgaac gaaatagaca gatcgctgag ataggtgcct cactgattaa gcattgggac 1380
aagagccacc cagaaacgct ggtgaaagta aaagatgctg aagatcagtt ggggtgcacga 1440
gtgggttaca tcgaactgga tctcaacagc ggtaagatcc ttgagagttt tcgccccgaa 1500
gaacgttttc caatgatgag cactttttaa gttctgctat gtggcgcggt attatcccgt 1560
gttgacgccc ggcaagagca actcggctgc cgcatacact attctcagaa tgacttggtt 1620
gagtactcac cagtcacaga aaagcatctt acggatggca tgacagtaag agaattatgc 1680
agtgtgcca taaccatgag tgataaact gcggccaact tacttctgac aacgatcgga 1740
ggaccgaagg agctaaccgc ttttttgcac aacatggggg atcatgtaac tcgccttgat 1800
cgttgggaac cggaactgaa tgaagccgcc gccaccatgg aaaacgccc gaaaggtgaa 1860
atcatgccga acatcccga gatgtccgct ttctggtatg ccgtgcgtac tgcggtgatc 1920
aacgccgcca gcggtcgta gactgtcgat gaagccctga aagacgcga gactcgtatc 1980
accaagtaa
1989

```

<210> 54

<211> 662

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
protein construct

<400> 54

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Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1             5             10             15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20             25             30

Leu Val Ile Trp Ile Asn Gly Leu Phe Gly Tyr Asn Gly Leu Ala Glu
      35             40             45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50             55             60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65             70             75             80

Asp Gly Pro Asp Ile Ile Phe Tyr Ala His Asp Arg Phe Gly Gly Tyr
      85             90             95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100            105            110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
      115            120            125

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Leu Ile Ala Tyr Pro Ile Ala Val Tyr Ala Leu Ser Leu Ile Tyr Asn  
 130 135 140  
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala  
 145 150 155 160  
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn  
 165 170 175  
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly  
 180 185 190  
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly  
 195 200 205  
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu  
 210 215 220  
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu  
 225 230 235 240  
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp  
 245 250 255  
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val  
 260 265 270  
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu  
 275 280 285  
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu  
 290 295 300  
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn  
 305 310 315 320  
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu  
 325 330 335  
 Leu Ala Lys Asp Pro Arg Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr  
 340 345 350  
 Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu  
 355 360 365  
 Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala  
 370 375 380  
 Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp  
 385 390 395 400  
 Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile  
 405 410 415  
 Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile  
 420 425 430

Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile  
           435                                  440                                  445  
 Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser His Pro  
           450                                  455                                  460  
 Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg  
  465                                  470                                  475                                  480  
 Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser  
                                   485                                  490                                  495  
 Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu  
                                   500                                  505                                  510  
 Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu  
                                   515                                  520                                  525  
 Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro  
                                   530                                  535                                  540  
 Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys  
  545                                  550                                  555                                  560  
 Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu  
                                   565                                  570                                  575  
 Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met  
                                   580                                  585                                  590  
 Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu  
                                   595                                  600                                  605  
 Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn  
                                   610                                  615                                  620  
 Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile  
  625                                  630                                  635                                  640  
 Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala  
                                   645                                  650                                  655  
 Gln Thr Arg Ile Thr Lys  
                                   660

&lt;210&gt; 55

&lt;211&gt; 662

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
           protein construct

&lt;400&gt; 55

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr  
   1                                  5                                  10                                  15



Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys  
                   20                                  25                                  30  
 Leu Val Ile Trp Ile Asn Gly Leu Gln Gly Tyr Asn Gly Leu Ala Glu  
                   35                                  40                                  45  
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu  
                   50                                  55                                  60  
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly  
                   65                                  70                                  75                                  80  
 Asp Gly Pro Asp Ile Ile Phe Tyr Ala His Asp Arg Phe Gly Gly Tyr  
                                   85                                  90                                  95  
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln  
                                   100                                  105                                  110  
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys  
                                   115                                  120                                  125  
 Leu Ile Ala Tyr Pro Ile Ala Val Gln Ala Leu Ser Leu Ile Tyr Asn  
                   130                                  135                                  140  
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala  
                   145                                  150                                  155                                  160  
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn  
                                   165                                  170                                  175  
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly  
                                   180                                  185                                  190  
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly  
                   195                                  200                                  205  
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu  
                   210                                  215                                  220  
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu  
                   225                                  230                                  235                                  240  
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp  
                                   245                                  250                                  255  
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val  
                                   260                                  265                                  270  
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu  
                   275                                  280                                  285  
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu  
                   290                                  295                                  300  
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn  
                   305                                  310                                  315                                  320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu  
                                   325                                  330                                  335

Leu Ala Lys Asp Pro Arg Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr  
                                   340                                  345                                  350

Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu  
                                   355                                  360                                  365

Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala  
                                   370                                  375                                  380

Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp  
 385                                  390                                  395                                  400

Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile  
                                   405                                  410                                  415

Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile  
                                   420                                  425                                  430

Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile  
                                   435                                  440                                  445

Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser His Pro  
                                   450                                  455                                  460

Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg  
 465                                  470                                  475                                  480

Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser  
                                   485                                  490                                  495

Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu  
                                   500                                  505                                  510

Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu  
                                   515                                  520                                  525

Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro  
                                   530                                  535                                  540

Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys  
 545                                  550                                  555                                  560

Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu  
                                   565                                  570                                  575

Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met  
                                   580                                  585                                  590

Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu  
                                   595                                  600                                  605

Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn  
                                   610                                  615                                  620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile  
625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala  
645 650 655

Gln Thr Arg Ile Thr Lys  
660

<210> 56

<211> 1989

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
nucleotide construct

<400> 56

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atgaaaataa aaacagggtgc acgcatcctc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcaag 120
gagggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccggtt agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctatgcacac gaccgctttg gtggctacgc tcaatctggc 300
ctggttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgca tcgctgttcg ggcgttatcg 420
ctgattttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggttaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggg atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa gggccaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaaac ccgccagtcc gaacaaagag 900
ctggcgaaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgtg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgtgcc aaccaaacga cgagcgtgac accacgatgc ctgcagcaat ggcaacaacg 1080
ttgcgcaaac tattaactgg cgaactactt actctagctt cccggcaaca attaatagac 1140
tggatggagg cggataaagt tgcaggacca cttctgcgct cggcccttcc ggctggctgg 1200
tttattgctg ataaatctgg agccggtgag cgtgggtctc gcggtatcat tgcagcactg 1260
gggccagatg gtaagccctc ccgtatcgta gttatctaca cgacggggag tcaggcaact 1320
atggatgaac gaaatagaca gatcgctgag ataggcgct cactgattaa gcattgggac 1380
aagagccacc cagaaacgct ggtgaaagta aaagatgctg aagatcagtt ggggtgcacg 1440
gtgggttaca tcgaactgga tctcaacagc ggtaagatcc ttgagagttt tcgccccgaa 1500
gaacgttttc caatgatgag cactttttaa gttctgctat gtggcgcggt attatcccgt 1560
gttgacgcgg ggcaagagca actcggtcgc cgcatacact attctcagaa tgacttggtt 1620
gagtactcac cagtcacaga aaagcatctt acggatggca tgacagtaag agaattatgc 1680
agtgtctgca taaccatgag tgataacact gcggccaact tacttctgac aacgatcgga 1740
ggaccgaagg agctaaccgc ttttttgcac aacatggggg atcatgtaac tcgccttgat 1800
cgttgggaac cggaactgaa tgaagccgcc gccaccatgg aaaacgccc gaaaggtgaa 1860
atcatgccga acatcccgc gatgtccgct ttctgggtat ccgtgcgtac tcgggtgatc 1920
aacgccgcca gcggtcgtca gactgtcgat gaagccctga aagacgcgca gactcgtatc 1980
accaagtaa 1989
```

&lt;210&gt; 57

&lt;211&gt; 662

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
protein construct

&lt;400&gt; 57

Met	Lys	Ile	Lys	Thr	Gly	Ala	Arg	Ile	Leu	Ala	Leu	Ser	Ala	Leu	Thr
1				5					10					15	

Thr	Met	Met	Phe	Ser	Ala	Ser	Ala	Leu	Ala	Lys	Ile	Glu	Glu	Gly	Lys
			20					25					30		

Leu	Val	Ile	Trp	Ile	Asn	Gly	Lys	Glu	Gly	Tyr	Asn	Gly	Leu	Ala	Glu
		35				40						45			

Val	Gly	Lys	Lys	Phe	Glu	Lys	Asp	Thr	Gly	Ile	Lys	Val	Thr	Val	Glu
	50					55					60				

His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	Pro	Gln	Val	Ala	Ala	Thr	Gly
65					70					75					80

Asp	Gly	Pro	Asp	Ile	Ile	Phe	Tyr	Ala	His	Asp	Arg	Phe	Gly	Gly	Tyr
				85					90					95	

Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	Thr	Pro	Asp	Lys	Ala	Phe	Gln
			100					105					110		

Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	Ala	Val	Arg	Tyr	Asn	Gly	Lys
		115					120					125			

Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Arg	Ala	Leu	Ser	Leu	Ile	Tyr	Asn
	130					135					140				

Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala
145					150					155					160

Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn
			165						170					175	

Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly
			180					185					190		

Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly
		195					200					205			

Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu
	210					215					220				

Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu
225					230					235					240

Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp
				245					250					255	

Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val  
 260 265 270  
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu  
 275 280 285  
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu  
 290 295 300  
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn  
 305 310 315 320  
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu  
 325 330 335  
 Leu Ala Lys Asp Pro Arg Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr  
 340 345 350  
 Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu  
 355 360 365  
 Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala  
 370 375 380  
 Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp  
 385 390 395 400  
 Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile  
 405 410 415  
 Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile  
 420 425 430  
 Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile  
 435 440 445  
 Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser His Pro  
 450 455 460  
 Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg  
 465 470 475 480  
 Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser  
 485 490 495  
 Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu  
 500 505 510  
 Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu  
 515 520 525  
 Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro  
 530 535 540  
 Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys  
 545 550 555 560

Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu  
565 570 575

Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met  
580 585 590

Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu  
595 600 605

Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn  
610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile  
625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala  
645 650 655

Gln Thr Arg Ile Thr Lys  
660

<210> 58

<211> 1989

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
nucleotide construct

<400> 58

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atgaaaataa aaacaggtgc acgcatcctc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcttg 120
gagggtctata acggtctcgc tgaagtcggg aagaaattcg agaaagatac cggaattaaa 180
gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctatgcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggtcg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttaccttg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgca tcgctgttcg tgcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgcaaaaaa cctgggaaga gatcccgcg 480
ctggataaag aactgaaagc gaaaggttaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcggtgat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggg atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgacctcaa gggtaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtc gaacaaagag 900
ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgtg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgtgcc aacaaaacga cgagcgtgac accacgatgc ctgcagcaat ggcaacaacg 1080
ttgcgcaaac tattaactgg cgaactactt actctagctt cccggcaaca attaatagac 1140
tggatggagg cggataaagt tgcaggacca cttctgcgct cggcccttcc ggctggctgg 1200
tttattgctg ataaatctgg agccggtgag cgtgggtctc gcggtatcat tgcagcactg 1260
gggccagatg gtaagccctc ccgtatcgta gttatctaca cgacggggag tcaggcaact 1320
atggatgaac gaaatagaca gatcgtgag ataggtgcct cactgattaa gcattgggac 1380
aagagccacc cagaaacgct ggtgaaagta aaagatgctg aagatcagtt gggcgacga 1440
gtgggttaca tcgaactgga tctcaacagc ggtaagatcc ttgagagttt tcgccccgaa 1500
gaacgttttc caatgatgag cacttttaaa gttctgctat gtggcgcggt attatcccgt 1560

```

```

gttgacgccg ggcaagagca actcgggtcgc cgcatacact attctcagaa tgacttgggtt 1620
gagtactcac cagtcacaga aaagcatctt acggatggca tgacagtaag agaattatgc 1680
agtgtctgcc taacctagag tgataacact gcggccaact tacttctgac aacgatcggg 1740
ggaccgaagg agctaaccgc ttttttgcac aacatggggg atcatgtaac tcgccttgat 1800
cgttgggaac cggaactgaa tgaagccgcc gccaccatgg aaaacgcca gaaagggtgaa 1860
atcatgccga acatcccga gatgtccgct ttctgggatg ccgtgcgtac tgcggtgatc 1920
aacgccgcca gcggtcgtca gactgtcgat gaagccctga aagacgcgca gactcgtatc 1980
accaagtaa                                     1989

```

<210> 59

<211> 662

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
protein construct

<400> 59

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1              5              10              15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20              25              30

Leu Val Ile Trp Ile Asn Gly Leu Glu Gly Tyr Asn Gly Leu Ala Glu
      35              40              45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50              55              60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65              70              75              80

Asp Gly Pro Asp Ile Ile Phe Tyr Ala His Asp Arg Phe Gly Gly Tyr
      85              90              95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100             105             110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
      115             120             125

Leu Ile Ala Tyr Pro Ile Ala Val Arg Ala Leu Ser Leu Ile Tyr Asn
      130             135             140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
      145             150             155             160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
      165             170             175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
      180             185             190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
      195             200             205

```

Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	210	215	220
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	225	230	235
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	245	250	255
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	260	265	270
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	275	280	285
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	290	295	300
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	305	310	315
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	325	330	335
Leu	Ala	Lys	Asp	Pro	Arg	Ala	Ile	Pro	Asn	Asp	Glu	Arg	Asp	Thr	Thr	340	345	350
Met	Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu	355	360	365
Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala	370	375	380
Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp	385	390	395
Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	405	410	415
Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	420	425	430
Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile	435	440	445
Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	His	Pro	450	455	460
Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	465	470	475
Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	485	490	495
Phe	Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	500	505	510



Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu  
 515 520 525

Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro  
 530 535 540

Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys  
 545 550 555 560

Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu  
 565 570 575

Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met  
 580 585 590

Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu  
 595 600 605

Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn  
 610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile  
 625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala  
 645 650 655

Gln Thr Arg Ile Thr Lys  
 660

<210> 60

<211> 1992

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 nucleotide construct

<400> 60

```

atgaaaataa aaacaggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
aaaggctata acggtctcgc tgaagtcggg aagaaattcg agaaagatac cggaattaaa 180
gtcacccgtt agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggtcg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgga tcgctgttga agcggttatc 420
ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccgcg 480
ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcggtgat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggg atggtccaac 780
atcgacacca gcaaagtga tttatggtga acggtactgc cgaccttcaa ggggtcaacca 840
tccaaaccgt tcggtggcgt gctgagcgca ggtattacg ccgccagtc gaacaaagag 900
ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020

```

```

ccacgctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg cggtatcatt 1080
gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac gacggggagt 1140
caggcaacta tggatgaacg aaatagacag atcgtctgaga taggtgcctc actgattaag 1200
cattggggat ccggcgggtg ccaccagaa acgctgggtga aagtaaaaga tgctgaagat 1260
cagttgggtg cacgagtggg ttacatcgaa ctggatctca acagcggtaa gatccttgag 1320
agttttcgcc ccgaagaacg ttttccaatg atgagcactt ttaaagttct gctatgtggc 1380
gcggtattat cccgtgttga cgccgggcaa gagcaactcg gtcgccgcat acactattct 1440
cagaatgact tggttgagta ctaccagtc acagaaaagc atcttacgga tggcatgaca 1500
gtaagagaat tatgcagtgc tgccataacc atgagtata acactgcggc caacttactt 1560
ctgacaacga tcggaggacc gaaggagcta accgcttttt tgcacaacat gggggatcat 1620
gtaactcgcc ttgatcggtg ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt 1680
gacaccacga tgcctgcagc aatggcaaca acgttgcgca aactattaac tggcgaacta 1740
cttactctag cttcccgga acaattaata gactggatgg aggcggataa agttgcagga 1800
ccacttctgc gtcggccct tccggctggc tccgccacca tggaaaacgc ccagaaaggt 1860
gaaatcatgc cgaacatccc gcagatgtcc gctttctggt atgccgtgcg tactgcggtg 1920
atcaacgccg ccagcggtcg tcagactgtc gatgaagccc tgaaagacgc gcagactcgt 1980
atcaccaagt aa 1992

```

<210> 61

<211> 663

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
protein construct

<400> 61

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1             5             10             15

```

```

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
          20             25             30

```

```

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
    35             40             45

```

```

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
    50             55             60

```

```

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
    65             70             75             80

```

```

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
          85             90             95

```

```

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
    100            105            110

```

```

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
    115            120            125

```

```

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
    130            135            140

```

```

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
    145            150            155            160

```

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn  
 165 170 175  
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly  
 180 185 190  
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly  
 195 200 205  
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu  
 210 215 220  
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu  
 225 230 235 240  
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp  
 245 250 255  
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val  
 260 265 270  
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu  
 275 280 285  
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu  
 290 295 300  
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn  
 305 310 315 320  
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu  
 325 330 335  
 Leu Ala Lys Asp Pro Arg Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly  
 340 345 350  
 Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys  
 355 360 365  
 Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met  
 370 375 380  
 Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys  
 385 390 395 400  
 His Trp Gly Ser Gly Gly Gly His Pro Glu Thr Leu Val Lys Val Lys  
 405 410 415  
 Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp  
 420 425 430  
 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe  
 435 440 445  
 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser  
 450 455 460

Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser  
465 470 475 480

Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr  
485 490 495

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser  
500 505 510

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys  
515 520 525

Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu  
530 535 540

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg  
545 550 555 560

Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu  
565 570 575

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp  
580 585 590

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro  
595 600 605

Ala Gly Ser Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro  
610 615 620

Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val  
625 630 635 640

Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp  
645 650 655

Ala Gln Thr Arg Ile Thr Lys  
660

<210> 62

<211> 1992

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
nucleotide construct

<400> 62

atgaaaataa aaacaggtgc acgcatactc gcattatccg cattaacgac gatgatgttt 60  
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaaactgg taatctggat taacggcgat 120  
aaaggctata acggtctcgc tgaagtcggg aagaaattcg agaaagatac cggaattaaa 180  
gtcaccggtt agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240  
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300  
ctgttgctg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttaacctg 360  
gatgccgtac gttacaacgg caagctgatt gcttaccgca tcgctgttga agcgttatcg 420  
ctgatttata acaaagatct gctgccgaac ccgcaaaaaa cctgggaaga gatcccggcg 480

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ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccgtgggc atggtccaac 780
atcgacacca gcaaagtga tttatgggtga acggtactgc cgaccttcaa ggggtcaacca 840
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aaagacaaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020
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gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac gacggggagt 1140
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cattggggat ccggcgggtg ccacccagaa acgctgggtga aagtaaaaga tgctgaagat 1260
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gcggtattat cccgtgttga cgccgggcaa gagcaactcg gtcgccgcat acactattct 1440
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gtaagagaat tatgcagtgc tgccataacc atgagtgata acactgcggc caacttactt 1560
ctgacaacga tcggaggacc gaaggagcta accgcttttt tgcacaacat ggggggatcat 1620
gtaactcgcc ttgatcgttg ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt 1680
gacaccacga tgcctgcagc aatggcaaca acgttgcgca aactattaac tggcgaacta 1740
cttactctag cttcccggca acaattaata gactggatgg aggcggataa agttgcagga 1800
ccacttctgc gtcggccct tccggctggc tccgccacca tggaaaacgc ccagaaaggt 1860
gaatggatgc cgaacatccc gcagatgtcc gctttctggt atgccgtgcg tactgcggtg 1920
atcaacgccg ccagcggtcg tcagactgtc gatgaagccc tgaaagacgc gcagactcgt 1980
atcaccaagt aa 1992

```

<210> 63

<211> 663

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic protein construct

<400> 63

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Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1              5              10              15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20              25              30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35              40              45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50              55              60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65              70              75              80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
      85              90              95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100              105              110

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Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	Ala	Val	Arg	Tyr	Asn	Gly	Lys	115	120	125
Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	Ala	Leu	Ser	Leu	Ile	Tyr	Asn	130	135	140
Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala	145	150	155
Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn	165	170	175
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly	180	185	190
Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	195	200	205
Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	210	215	220
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	225	230	235
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	245	250	255
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	260	265	270
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	275	280	285
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	290	295	300
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	305	310	315
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	325	330	335
Leu	Ala	Lys	Asp	Pro	Arg	Trp	Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	340	345	350
Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	355	360	365
Pro	Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	370	375	380
Asp	Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	385	390	395
His	Trp	Gly	Ser	Gly	Gly	Gly	His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	405	410	415

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp  
 420 425 430  
 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe  
 435 440 445  
 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser  
 450 455 460  
 Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser  
 465 470 475 480  
 Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr  
 485 490 495  
 Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser  
 500 505 510  
 Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys  
 515 520 525  
 Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu  
 530 535 540  
 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg  
 545 550 555 560  
 Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu  
 565 570 575  
 Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp  
 580 585 590  
 Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro  
 595 600 605  
 Ala Gly Ser Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Trp Met Pro  
 610 615 620  
 Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val  
 625 630 635 640  
 Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp  
 645 650 655  
 Ala Gln Thr Arg Ile Thr Lys  
 660

<210> 64

<211> 1992

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
nucleotide construct

&lt;400&gt; 64

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tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccggtg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggttg aaatcacccc ggacaaagcg ttcaggaca agctgtatcc gtttacctgg 360
gattgggtac gttacaacgg caagctgatt gcttaccoga tgcgtgttga agcgttatcg 420
ctgattttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccgcg 480
ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
aagtagcaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggg atggtccaac 780
atcgacacca gcaaagtga tttatggtgta acggtactgc cgaccttcaa gggcacaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtc gaacaaagag 900
ctggcgaaaag agttcctcga aaactatctg ctgactgatg aaggctctga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgtg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgctggg ttattgctga taaatctgga gccggtgagc gtgggtctcg cggatcatt 1080
gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac gacggggagt 1140
caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc actgattaag 1200
cattggggat ccggcgggtg ccacccagaa acgctgggtg aagtaaaaga tgctgaagat 1260
cagttgggtg cacgagtggg ttacatcgaa ctggatctca acagcggtaa gatccttgag 1320
agttttcgcc ccgaagaacg ttttccaatg atgagcactt ttaaagttct gctatgtggc 1380
gcggtattat ccggtgttga cgccgggcaa gagcaactcg gtgcgcgat acactattct 1440
cagaatgact tgggtgagta ctaccagtc acagaaaagc atcttacgga tggcatgaca 1500
gtaagagaat tatgcagtgc tgccataacc atgagtgata aactgcggc caacttactt 1560
ctgacaacga tcggaggacc gaaggagcta accgcttttt tgcacaacat gggggatcat 1620
gtaactcgcc ttgatcggtg ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt 1680
gacaccacga tgctgcagc aatggcaaca acgttgcgca aactattaac tggcgaacta 1740
cttactctag cttcccggca acaattaata gactggatgg aggcggataa agttgcagga 1800
ccacttctgc gctcgccct tccggctggc tccgccacca tggaaaacgc ccagaaaggt 1860
gaatggatgc cgaacatccc gcagatgtcc gctttctggt atgccgtgcg tactgcggtg 1920
atcaacgccg ccagcggtcg tcagactgtc gatgaagccc tgaaagacgc gcagactcgt 1980
atcaccaagt aa 1992

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&lt;210&gt; 65

&lt;211&gt; 663

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
protein construct

&lt;400&gt; 65

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Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1             5             10             15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
          20             25             30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
          35             40             45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
          50             55             60

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His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly  
 65 70 75 80  
 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr  
 85 90 95  
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln  
 100 105 110  
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Trp Val Arg Tyr Asn Gly Lys  
 115 120 125  
 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn  
 130 135 140  
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala  
 145 150 155 160  
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn  
 165 170 175  
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly  
 180 185 190  
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly  
 195 200 205  
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu  
 210 215 220  
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu  
 225 230 235 240  
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp  
 245 250 255  
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val  
 260 265 270  
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu  
 275 280 285  
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu  
 290 295 300  
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn  
 305 310 315 320  
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu  
 325 330 335  
 Leu Ala Lys Asp Pro Arg Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly  
 340 345 350  
 Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys  
 355 360 365

Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met  
 370 375 380  
 Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys  
 385 390 395 400  
 His Trp Gly Ser Gly Gly Gly His Pro Glu Thr Leu Val Lys Val Lys  
 405 410 415  
 Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp  
 420 425 430  
 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe  
 435 440 445  
 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser  
 450 455 460  
 Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser  
 465 470 475 480  
 Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr  
 485 490 495  
 Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser  
 500 505 510  
 Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys  
 515 520 525  
 Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu  
 530 535 540  
 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg  
 545 550 555 560  
 Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu  
 565 570 575  
 Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp  
 580 585 590  
 Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro  
 595 600 605  
 Ala Gly Ser Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Trp Met Pro  
 610 615 620  
 Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val  
 625 630 635 640  
 Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp  
 645 650 655  
 Ala Gln Thr Arg Ile Thr Lys  
 660

<210> 66  
 <211> 1989  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 nucleotide construct

<400> 66  
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 aaaggctata acgggtctcgc tgaagtccgtt aagaaattcg agaaagatac cggaattaaa 180  
 gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240  
 gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300  
 ctggttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360  
 gatgccgtac gttacaacgg caagctgatt gcttaccgga tcgctgttga agcgttatcg 420  
 ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480  
 ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540  
 tacttcacct ggccgctgat tgctgctgac gggcatctta cggatggcat gacagtaaga 600  
 gaattatgca gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca 660  
 acgatcggag gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact 720  
 cgccttgatc gttgggaacc ggaactgaat gaagccatac caaacgacga gcgtgacacc 780  
 acgatgcctg cagcaatggc aacaacgttg cgcaaaactat taactggcga actacttact 840  
 ctagcttccc ggcaacaatt aatagactgg atggaggcgg ataaagtgc aggaccactt 900  
 ctgcgctcgg cccttcgggc tggctggttt attgctgata aatctggagc cgggtgagcgt 960  
 ggggtctcgg gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagtt 1020  
 atctacacga cggggagtcg ggcaactatg gatgaacgaa atagacagat cgctgagata 1080  
 ggtgcctcac tgattaagca ttgggacaag agccacccag aaacgctggt gaaagtaaaa 1140  
 gatgctgaag atcagttggg tgcacgagtg gggtacatcg aactggatct caacagcggt 1200  
 aagatccttg agagttttcg ccccgaagaa cgttttccaa tgatgagcac ttttaaagtt 1260  
 ctgctatgtg gcgcggtatt atcccgtgtt gacgcggggc aagagcaact cggctcgccgc 1320  
 atacactatt ctccagaatga cttggttgag tactcaccag tcacagacgg gggttatgcg 1380  
 ttcaagtatg aaaacggcaa gtacgacatt aaagacgtgg gcgtggataa cgctggcgcg 1440  
 aaagcgggtc tgaccttctt ggttgacctg attaaaaaca aacacatgaa tgcagacacc 1500  
 gattactcca tcgcagaagc tgctttaa ataaaggcga cagcgatgac catcaacggc 1560  
 ccgtgggcat ggtccaacat cgacaccagc aaagtgaatt atggtgtaac ggtactgccc 1620  
 accttcaagg gtcaaccatc caaacggttc gttggcgtgc tgagcgcagg tattaacgcc 1680  
 gccagtccga acaaagagct ggcgaaagag ttctcga aaactatctgct gactgatgaa 1740  
 ggtctggaag cggttaataa agacaaaccg ctgggtgccg tagcgtgaa gtcttacgag 1800  
 gaagagttgg cgaaagatcc acgtattgcc gccaccatgg aaaacgcccc gaaaggtgaa 1860  
 atcatgccga acatcccgcg gatgtccgct ttctggtatg ccgtgcgtac tgcggtgatc 1920  
 aacgcgcgca gcggtcgtca gactgtcgat gaagccctga aagacgcgca gactcgtatc 1980  
 accaagtaaa 1989

<210> 67  
 <211> 662  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 protein construct

<400> 67  
 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr  
 1 5 10 15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys  
                   20                                  25                                  30  
 Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu  
                   35                                  40                                  45  
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu  
                   50                                  55                                  60  
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly  
                   65                                  70                                  75                                  80  
 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr  
                                   85                                  90                                  95  
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln  
                                   100                                  105                                  110  
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys  
                   115                                  120                                  125  
 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn  
                   130                                  135                                  140  
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala  
                   145                                  150                                  155                                  160  
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn  
                                   165                                  170                                  175  
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly His  
                                   180                                  185                                  190  
 Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr  
                   195                                  200                                  205  
 Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly  
                   210                                  215                                  220  
 Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr  
                   225                                  230                                  235                                  240  
 Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp  
                                   245                                  250                                  255  
 Glu Arg Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys  
                   260                                  265                                  270  
 Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile  
                   275                                  280                                  285  
 Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala  
                   290                                  295                                  300  
 Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg  
                   305                                  310                                  315                                  320

Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser  
 325 330 335  
 Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu  
 340 345 350  
 Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp  
 355 360 365  
 Asp Lys Ser His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp  
 370 375 380  
 Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly  
 385 390 395 400  
 Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser  
 405 410 415  
 Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala  
 420 425 430  
 Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu  
 435 440 445  
 Val Glu Tyr Ser Pro Val Thr Asp Gly Gly Tyr Ala Phe Lys Tyr Glu  
 450 455 460  
 Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala  
 465 470 475 480  
 Lys Ala Gly Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met  
 485 490 495  
 Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly  
 500 505 510  
 Glu Thr Ala Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp  
 515 520 525  
 Thr Ser Lys Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly  
 530 535 540  
 Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala  
 545 550 555 560  
 Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu  
 565 570 575  
 Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly  
 580 585 590  
 Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg  
 595 600 605  
 Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn  
 610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile  
 625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala  
 645 650 655

Gln Thr Arg Ile Thr Lys  
 660

<210> 68  
 <211> 1995  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 nucleotide construct

<400> 68  
 atgaaaataa aaacaggtgc acgcatcctc gcattatccg cattaacgac gatgatgttt 60  
 tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120  
 aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180  
 gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240  
 gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300  
 ctggttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360  
 gatgccgtac gttacaacgg caagctgatt gcttaccgca tcgctggtga agcgttatcg 420  
 ctgatttata acaaagatct gctgccgaac ccgcaaaaaa cctgggaaga gatcccggcg 480  
 ctggataaag aactgaaagc gaaaggtaa agcgcgctga tgttcaacct gcaagaaccg 540  
 tacttcacct ggccgctgat tgctgctgac gggcttctgc gctcgccct tccggctggc 600  
 tggtttattg ctgataaatc tggagccggt gagcgtgggt ctgcggtat cattgcagca 660  
 ctggggccag atggtaagcc ctcccgtatc gtagtattct acacgacggg gagttaggca 720  
 actatggatg aacgaaatag acagatcgct gagatagggt cctcactgat taagcattgg 780  
 ggatccggcg gtggccaccc agaaacgctg gtgaaagtaa aagatgctga agatcagttg 840  
 ggtgcacgag tgggttacat cgaactggat ctcaacagcg gtaagatcct tgagagtttt 900  
 cgccccgaag aacgttttcc aatgatgagc acttttaaag ttctgctatg tggcgcggtg 960  
 ttatcccgtg ttgacgccgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat 1020  
 gacttggttg agtactcacc agtcacagaa aagcatctta cggatggcat gacagtaaga 1080  
 gaattatgca gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca 1140  
 acgatcggag gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact 1200  
 cgccttgatc gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc 1260  
 acgatgcctg cagcaatggc aacaacgttg cgaaactat taactggcga actacttact 1320  
 ctagcttccc ggcaacaatt aatagactgg atggagcgcg ataaagtgc agacgggggt 1380  
 tatgcgttca agtatgaaaa cggcaagtac gacattaaag acgtgggcgt ggataacgct 1440  
 ggcgcgaaag cgggtctgac cttcctggtt gacctgatta aaaacaaaca catgaatgca 1500  
 gacaccgatt actccatcgc agaagctgcc tttaataaag gcgaaacagc gatgaccatc 1560  
 aacggccccgt gggcatggtc caacatcgac accagcaaag tgaattatgg tgtaacggta 1620  
 ctgccgacct tcaagggta accatccaaa ccgttcgttg gcgtgctgag cgcagggtatt 1680  
 aacgcccga gtccgaacaa agagctggcg aaagagttcc tcgaaaacta tctgctgact 1740  
 gatgaagggtc tggaaagcgt taataaagac aaaccgctgg gtgccgtagc gctgaagtct 1800  
 tacgaggaag agttggcgaa agatccacgt attgccgcca ccatggaaaa cggccagaaa 1860  
 ggtgaaatca tgccgaacat cccgcagatg tccgctttct ggtatgccgt gcgtactgcg 1920  
 gtgatcaacg ccgccagcgg tcgtcagact gtcgatgaag ccctgaaaga cgcgcagact 1980  
 cgtatcacca agtaa 1995

&lt;210&gt; 69

&lt;211&gt; 664

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic protein construct

&lt;400&gt; 69

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr  
 1 5 10 15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys  
 20 25 30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu  
 35 40 45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu  
 50 55 60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly  
 65 70 75 80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr  
 85 90 95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln  
 100 105 110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys  
 115 120 125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn  
 130 135 140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala  
 145 150 155 160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn  
 165 170 175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Leu  
 180 185 190

Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly  
 195 200 205

Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp  
 210 215 220

Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala  
 225 230 235 240

Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu  
 245 250 255

Ile	Lys	His	Trp	Gly	Ser	Gly	Gly	Gly	His	Pro	Glu	Thr	Leu	Val	Lys	260	265	270	
Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr	Ile	Glu	275	280	285	
Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe	Arg	Pro	Glu	Glu	290	295	300	
Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu	Cys	Gly	Ala	Val	305	310	315	320
Leu	Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly	Arg	Arg	Ile	His	325	330	335	
Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val	Thr	Glu	Lys	His	340	345	350	
Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser	Ala	Ala	Ile	Thr	355	360	365	
Met	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	Thr	Thr	Ile	Gly	Gly	370	375	380	
Pro	Lys	Glu	Leu	Thr	Ala	Phe	Leu	His	Asn	Met	Gly	Asp	His	Val	Thr	385	390	395	400
Arg	Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu	Asn	Glu	Ala	Ile	Pro	Asn	Asp	405	410	415	
Glu	Arg	Asp	Thr	Thr	Met	Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	420	425	430	
Leu	Leu	Thr	Gly	Glu	Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	435	440	445	
Asp	Trp	Met	Glu	Ala	Asp	Lys	Val	Ala	Asp	Gly	Gly	Tyr	Ala	Phe	Lys	450	455	460	
Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	465	470	475	480
Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	485	490	495	
His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	500	505	510	
Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	515	520	525	
Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	530	535	540	
Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	Ser	Ala	Gly	Ile	545	550	555	560



Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn  
565 570 575

Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro  
580 585 590

Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp  
595 600 605

Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met  
610 615 620

Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala  
625 630 635 640

Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys  
645 650 655

Asp Ala Gln Thr Arg Ile Thr Lys  
660

<210> 70

<211> 2004

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
nucleotide construct

<400> 70

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atgaaaataa aaacaggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaaactgg taatctggat taacggcgat 120
aaaggctata acggtctcgc tgaagtcggg aagaaattcg agaaagatac cggaattaaa 180
gtcacccgtt agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggttg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgca tcgctgttga agcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgcaaaaaa cctgggaaga gatcccgcg 480
ctggataaag aactgaaagc gaagagtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac gggaatgaag ccataccaaa cgacgagcgt 600
gacaccacga tgcctgcagc aatggcaaca acgttgcgca aactattaac tggcgaacta 660
cttactctag cttcccgcca acaattaata gactggatgg aggcggataa agttgcagga 720
ccacttctgc gctcgccctt tccggctggc tggtttattg ctgataaatc tggagccggg 780
gagcgtgggt ctgcggtat cattgcagca ctggggccag atggtaagcc ctcccgtatc 840
gtagttatct acacgacggg gagtcaggca actatggatg aacgaaatag acagatcgct 900
gagatagggt cctcactgat taagcattgg gacaagagcc acccagaaac gctggtgaaa 960
gtaaaagatg ctgaagatca gttgggtgca cgagtgggtt acatcgaact ggatctcaac 1020
agcggtaaga tccttgagag ttttcgcccc gaagaacggt ttccaatgat gacactttt 1080
aaagttctgc tatgtggcgc ggtattatcc cgtgttgacg ccgggcaaga gcaactcggg 1140
cgccgcatac actattctca gaatgacttg gttgagtact caccagtcac agaaaagcat 1200
cttacggatg gcatgacagt aagagaatta tgcagtgctg ccataaccat gagtgataac 1260
actgcggcca acttacttct gacaacgatc ggaggaccga aggagctaac cgcttttttg 1320
cacaacatgg gggatcatgt aactgcctt gatcggtggg aaccggaact gaatgaagcc 1380
gacggggggt atcggttcaa gtatgaaaac ggcaagtacg acattaaaga cgtgggcgtg 1440
gataacgctg gcgcgaaagc gggctctgacc ttctgtgttg acctgattaa aaacaaacac 1500
atgaatgcag acaccgatta ctccatcgca gaagctgcct ttaataaagg cgaaacagcg 1560

```

```

atgaccatca acggcccgtg ggcattggtcc aacatcgaca ccagcaaagt gaattatggt 1620
gtaacgggtac tgccgacctt caaggggtcaa ccatccaaac cgttcgttgg cgtgctgagc 1680
gcaggtatta acgccgccag tccgaacaaa gagctggcga aagagttcct cgaaaactat 1740
ctgctgactg atgaaggtct ggaagcgggt aataaagaca aaccgctggg tgccgtagcg 1800
ctgaagtctt acgaggaaga gttggcgaaa gatccacgta ttgccgccac catggaaaac 1860
gcccagaaaag gtgaaatcat gccgaacatc ccgcagatgt ccgctttctg gtatgccgtg 1920
cgtactgcgg tgatcaacgc cgccagcggg cgtcagactg tcgatgaagc cctgaaagac 1980
gcgcagactc gtatcaccaa gtaa                                     2004

```

<210> 71

<211> 667

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
protein construct

<400> 71

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1              5              10              15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20              25              30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35              40              45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50              55              60

His Pro Asp Lys Leu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65              70              75              80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
      85              90              95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100             105             110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
      115             120             125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
      130             135             140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
      145             150             155             160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
      165             170             175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Asn
      180             185             190

Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Ala Ala Met
      195             200             205

```

Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala  
 210 215 220  
 Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly  
 225 230 235 240  
 Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys  
 245 250 255  
 Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly  
 260 265 270  
 Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser  
 275 280 285  
 Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala  
 290 295 300  
 Ser Leu Ile Lys His Trp Asp Lys Ser His Pro Glu Thr Leu Val Lys  
 305 310 315 320  
 Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu  
 325 330 335  
 Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu  
 340 345 350  
 Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val  
 355 360 365  
 Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His  
 370 375 380  
 Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His  
 385 390 395 400  
 Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr  
 405 410 415  
 Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly  
 420 425 430  
 Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr  
 435 440 445  
 Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Asp Gly Gly Tyr  
 450 455 460  
 Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly Val  
 465 470 475 480  
 Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu Ile  
 485 490 495  
 Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu Ala  
 500 505 510

Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp Ala  
515 520 525

Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val Leu  
530 535 540

Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser  
545 550 555 560

Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe  
565 570 575

Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys  
580 585 590

Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu  
595 600 605

Ala Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly  
610 615 620

Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val  
625 630 635 640

Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu  
645 650 655

Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys  
660 665

<210> 72

<211> 2001

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
nucleotide construct

<400> 72

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atgaaaataa aaacaggtgc acgcatactc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccggtg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggtcg aaatcacccc ggacaaaagcgt ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgga tcgctgttga agcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgcaaaaaa cctgggaaga gatcccggcg 480
ctggataaaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac gggggttatg cggtcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggg atggtccaac 780
atcgacacca gcaaagtga tttatggtga acggtactgc cgaccttcaa gggccaacca 840
tccaaacgct tcggtggcgt gctgagcgca ggtattaacg ccgccagtc gaacaaagag 900
ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020
```

```

ccacgtattg cgcgccacat ggaaaacgcc cagaaagggtg aaatcatgcc gaacatccccg 1080
cagatgtccg ctttctggta tgccgtgcgt actgcgggtga tcaacgccgc cagcgggtcgt 1140
cagactgtcg atgaagccct gaaagacgcg cagactcgta tcaccaaggg catgacagta 1200
agagaattat gcagtgtgc cataaccatg agtgataaca ctgcggccaa cttactttctg 1260
acaacgatcg gaggaccgaa ggagctaacc gcttttttgc acaacatggg ggatcatgta 1320
actcgccttg atcgttggga accggagctg aatgaagcca taccaaacga cgagcgtgac 1380
accacgatgc ctgcagcaat ggcaacaacg ttgcgcaaac tattaactgg cgaactactt 1440
actctagctt cccggcaaca attaatagac tggatggagg cggataaagt tgcaggacca 1500
cttctgcgct cggcccttcc ggctggctgg tttattgctg ataaatctgg agccggtgag 1560
cgtgggtctc gcggtatcat tgcagcactg gggccagatg gtaagccctc ccgtatcgta 1620
gttatctaca cgacggggag tcaggcaact atggatgaac gaaatagaca gatcgctgag 1680
ataggtgcct cactgattaa gcattgggga tccggcggtg gccaccaga aacgctggtg 1740
aaagtaaaag atgctgaaga tcagttgggt gcacgagtgg gttacatcga actggatctc 1800
aacagcggta agatccttga gagttttcgc cccgaagaac gttttccaat gatgagcact 1860
tttaaagttc tgctatgtgg cgcgttatta tcccgtgttg acgccgggca agagcaactc 1920
ggtcgccgca tacactattc tcagaatgac ttggttgagt actcaccagt cacagaaaag 1980
catcttacgg atggcaagtg a                                     2001

```

<210> 73

<211> 666

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
protein construct

<400> 73

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1             5             10             15

```

```

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
          20             25             30

```

```

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
          35             40             45

```

```

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
          50             55             60

```

```

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
          65             70             75             80

```

```

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
          85             90             95

```

```

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
          100            105            110

```

```

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
          115            120            125

```

```

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
          130            135            140

```

```

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
          145            150            155            160

```

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn  
 165 170 175  
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly  
 180 185 190  
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly  
 195 200 205  
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu  
 210 215 220  
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu  
 225 230 235 240  
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp  
 245 250 255  
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val  
 260 265 270  
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu  
 275 280 285  
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu  
 290 295 300  
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn  
 305 310 315 320  
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu  
 325 330 335  
 Leu Ala Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys  
 340 345 350  
 Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala  
 355 360 365  
 Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp  
 370 375 380  
 Glu Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys Gly Met Thr Val  
 385 390 395 400  
 Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala  
 405 410 415  
 Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe  
 420 425 430  
 Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro  
 435 440 445  
 Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro  
 450 455 460

Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu  
 465 470 475 480

Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys  
 485 490 495

Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile  
 500 505 510

Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala  
 515 520 525

Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr  
 530 535 540

Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu  
 545 550 555 560

Ile Gly Ala Ser Leu Ile Lys His Trp Gly Ser Gly Gly Gly His Pro  
 565 570 575

Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg  
 580 585 590

Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser  
 595 600 605

Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu  
 610 615 620

Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu  
 625 630 635 640

Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro  
 645 650 655

Val Thr Glu Lys His Leu Thr Asp Gly Lys  
 660 665

&lt;210&gt; 74

&lt;211&gt; 2010

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 nucleotide construct

&lt;400&gt; 74

atgaaaataa aaacaggtgc acgcatactc gcattatccg cattaacgac gatgatgttt 60  
 tccgctcgg ctctcgccaa aatcgaagaa ggtaaaactgg taatctggat taacggcgat 120  
 aaaggctata acggtctcgc tgaagtcggg aagaaattcg agaaagatac cggaattaaa 180  
 gtcaccggtg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240  
 gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300  
 ctgttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360  
 gatgccgtac gttacaacgg caagctgatt gcttaccgga tcgctgttga agcgttatcg 420  
 ctgatttata acaaagatct gctgccgaac ccgcaaaaaa cctgggaaga gatcccggtg 480

```

ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtagat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccgtgggc atggtccaac 780
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cagatgtccg ctttctggta tgccgtgcgt actgcgggtg tcaacgccgc cagcggtcgt 1140
cagactgtcg atgaagccct gaaagacgcg cagactcgta tcaccaaggg catgacagta 1200
agagaattat gcagtgtctc cataaccatg agtgataaca ctgcggccaa cttacttctg 1260
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actctagctt cccggcaaca attaatagac tggatggagg cggataaagt tgcaggacca 1500
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cgtgggtctc gcggtatcat tgcagcactg gggccagatg gtaagccctc ccgtatcgta 1620
gttatctaca cgacggggag tcaggcaact atggatgaac gaaatagaca gatcgtgag 1680
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tttaaagttc tgctatgtgg cgcggtatta tcccggtgtg acgccgggca agagcaactc 1920
ggtcgccgca tacactattc tcagaatgac ttggttgagt actcaccagt cacagaaaag 1980
catcttacgg aagtgaagag cactagttag                2010

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<210> 75

<211> 669

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
protein construct

<400> 75

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Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1                      5                      10                      15

```

```

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
                20                      25                      30

```

```

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
  35                      40                      45

```

```

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
  50                      55                      60

```

```

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
  65                      70                      75                      80

```

```

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
                85                      90                      95

```

```

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
  100                      105                      110

```



Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys  
 115 120 125  
 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn  
 130 135 140  
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala  
 145 150 155 160  
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn  
 165 170 175  
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly  
 180 185 190  
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly  
 195 200 205  
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu  
 210 215 220  
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu  
 225 230 235 240  
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp  
 245 250 255  
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val  
 260 265 270  
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu  
 275 280 285  
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu  
 290 295 300  
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn  
 305 310 315 320  
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu  
 325 330 335  
 Leu Ala Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys  
 340 345 350  
 Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala  
 355 360 365  
 Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp  
 370 375 380  
 Glu Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys Gly Met Thr Val  
 385 390 395 400  
 Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala  
 405 410 415

Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe  
 420 425 430  
 Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro  
 435 440 445  
 Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro  
 450 455 460  
 Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu  
 465 470 475 480  
 Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys  
 485 490 495  
 Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile  
 500 505 510  
 Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala  
 515 520 525  
 Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr  
 530 535 540  
 Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu  
 545 550 555 560  
 Ile Gly Ala Ser Leu Ile Lys His Trp Gly Ser Gly Gly Gly His Pro  
 565 570 575  
 Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg  
 580 585 590  
 Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser  
 595 600 605  
 Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu  
 610 615 620  
 Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu  
 625 630 635 640  
 Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro  
 645 650 655  
 Val Thr Glu Lys His Leu Thr Glu Val Lys Ser Thr Ser  
 660 665

<210> 76

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 76  
ggaccaggat ccatgaaaat aaaaacaggt

30

<210> 77  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<400> 77  
Gly Gly Ser Gly His His His His His His His  
1 5 10

<210> 78  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 78  
gctctttctca cccagaaacg ctggtg

26

<210> 79  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 79  
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35

<210> 80  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 80  
cacccagaaa cgctggtg

18

<210> 81  
<211> 24  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 81  
ctgattaagc attgggacaa gagc

24

<210> 82  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 82  
gtggctcttg tcccaatgct taatcag

27

<210> 83  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 83  
caccagcggt tctgg

15

<210> 84  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 84  
ctgattaagc attgggacaa gagccacca gaaacgtgg tg

42

<210> 85  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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 <400> 85  
 ggatccggcg gtggccaccc agaaacgctg gtg 33  
  
 <210> 86  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide  
  
 <400> 86  
 ctgattaagc attggggatc c 21  
  
 <210> 87  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide  
  
 <400> 87  
 gatccggcgg tggccaccca gaaacgctgg tg 32  
  
 <210> 88  
 <211> 16  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide  
  
 <400> 88  
 ctgattaagc attggg 16  
  
 <210> 89  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Description of Artificial Sequence: Synthetic  
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 <400> 89  
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<210> 90  
 <211> 28  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 90  
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28

<210> 91  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 91  
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48

<210> 92  
 <211> 59  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 92  
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<210> 93  
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 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 93  
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15

<210> 94  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 94

gacgggggtt atgcgttc

18

<210> 95

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 95

gaacgcataa ccccc

15

<210> 96

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 96

cccgtcagca gcaatcag

18

<210> 97

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 97

ctgattgctg ctgacggg

18

<210> 98

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 98  
ctgatcgcta ggagacggcg a

21

<210> 99  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
6xHis tag

<400> 99  
His His His His His His  
1 5